

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
1	471	100.0	471	4	US-08-931-858E-203	Sequence 203, App	
c	2	471	100.0	471	4	US-08-931-858E-204	Sequence 204, App
3	487.8	99.3	471	4	US-08-931-858E-205	Sequence 205, App	
c	4	487.8	99.3	471	4	US-08-931-858E-206	Sequence 206, App
5	291	61.8	291	4	US-08-931-858E-199	Sequence 199, App	
c	6	291	61.8	291	4	US-08-931-858E-200	Sequence 200, App
7	289.4	61.4	291	4	US-08-931-858E-201	Sequence 201, App	
c	8	289.4	61.4	291	4	US-08-931-858E-202	Sequence 202, App
9	267	56.7	267	4	US-08-931-858E-222	Sequence 222, App	
10	250	53.1	471	4	US-08-931-858E-179	Sequence 179, App	
c	11	250	53.1	471	4	US-08-931-858E-180	Sequence 180, App
12	250	53.1	471	4	US-08-931-858E-190	Sequence 190, App	
c	13	250	53.1	471	4	US-08-931-858E-191	Sequence 191, App
14	207.6	44.1	405	4	US-08-981-739E-175	Sequence 175, App	
15	207.6	44.1	405	4	US-09-128-026E-175	Sequence 175, App	
16	207.6	44.1	544	4	US-08-931-858E-105	Sequence 105, App	
17	207.6	44.1	544	4	US-08-981-739E-105	Sequence 105, App	
18	207.6	44.1	544	4	US-09-128-026E-105	Sequence 105, App	
19	207.6	44.1	559	4	US-08-931-858E-131	Sequence 131, App	
20	207.6	44.1	559	4	US-08-981-739E-131	Sequence 131, App	
21	207.6	44.1	559	4	US-09-128-026E-131	Sequence 131, App	
22	207.6	44.1	723	4	US-08-931-858E-177	Sequence 177, App	
c	23	207.6	44.1	723	4	US-08-931-858E-178	Sequence 178, App
24	203	43.1	559	4	US-08-931-858E-188	Sequence 188, App	
c	25	203	43.1	559	4	US-08-931-858E-189	Sequence 189, App
26	203	43.1	559	4	US-08-981-739E-134	Sequence 134, App	
27	203	43.1	559	4	US-09-128-026E-134	Sequence 134, App	

ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-931-858E-199

Query Match 61.8%; Score 291; DB 4; Length 291;

Best Local Similarity 100.0%; Pred. No. 7e-53;

Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GCCCTGTCTGTCATGCCAGCTGTGAGCCTGACCCCTGTCGCTGGCAGAGCTAGGCCCTG 240
Db 1 GCCCTGTCTGTCATGCCAGCTGTGAGCCTGACCCCTGTCGCTGGCAGAGCTAGGCCCTG 60
QY 241 GCTACGCTCAGAGGAGAGGTCATCTCCGCTACTGCGCGGCGAGCTGCCCGCGTGT 300
Db 61 GCTACGCTCAGAGGAGAGGTCATCTCCGCTACTGCGCGGCGAGCTGCCCGCGTGT 120
QY 301 GCCCGCACCCAGCATGGCTGGCGCTGGCGGCTGCAGGGCCAGGGCCGAGCCACACG 360
Db 121 GCCCGCACCCAGCATGGCTGGCGCTGGCGGCTGCAGGGCCAGGGCCGAGCCACACG 180
QY 361 GGGCCCTCTCGCGGCCCACTCGCTACACGAGTGGCTTCTCGATGACGGCCACGCG 420
Db 181 GGGCCCTCTCGCGGCCCACTCGCTACACGAGTGGCTTCTCGATGACGGCCACGCG 240
QY 421 TGGCAGCGGCTGCCCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTG 471
Db 241 TGGCAGCGGCTGCCCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTG 291

RESULT 6

US-08-931-858E-200/G

Sequence 200, Application US/08931858E

Patent No. 622022

GENERAL INFORMATION:

APPLICANT: JOHNSON, EUGENE M

APPLICANT: MILBRANDT, JEFFREY D

APPLICANT: KOTZBAUER, PAUL T

APPLICANT: LAMPE, PATRICIA A

APPLICANT: KLEIN, ROBERT

APPLICANT: DESAUVAGE, FRED

TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAFERKAMP, L.C.

STREET: 7733 FORSYTH BOULEVARD, SUITE 1400

CITY: ST. LOUIS

STATE: MO

COUNTRY: USA

ZIP: 63105

STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-931-858E-200

Query Match 61.8%; Score 291; DB 4; Length 291;

Best Local Similarity 100.0%; Pred. No. 7e-53;

Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GCCCTGTCTGTCATGCCAGCTGTGAGCCTGACCCCTGTCGCTGGCAGAGCTAGGCCCTG 240
Db 291 GCCCTGTCTGTCATGCCAGCTGTGAGCCTGACCCCTGTCGCTGGCAGAGCTAGGCCCTG 232
QY 241 GCTACGCTCAGAGGAGAGGTCATCTCCGCTACTGCGCGGCGAGCTGCCCGCGTGT 300
Db 231 GCTACGCTCAGAGGAGAGGTCATCTCCGCTACTGCGCGGCGAGCTGCCCGCGTGT 172
QY 301 GCCCGCACCCAGCATGGCTGGCGCTGGCGGCTGCAGGGCCAGGGCCGAGCCACACG 360
Db 171 GCCCGCACCCAGCATGGCTGGCGCTGGCGGCTGCAGGGCCAGGGCCGAGCCACACG 112
QY 361 GGGCCCTCTCGCGGCCCACTCGCTACACGAGTGGCTTCTCGATGACGGCCACGCG 420
Db 111 GGGCCCTCTCGCGGCCCACTCGCTACACGAGTGGCTTCTCGATGACGGCCACGCG 52
QY 421 TGGCAGCGGCTGCCCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTG 471
Db 51 TGGCAGCGGCTGCCCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTG 1

RESULT 7

US-08-931-858E-201

Sequence 201, Application US/08931858E

Patent No. 622022

GENERAL INFORMATION:

APPLICANT: JOHNSON, EUGENE M

APPLICANT: MILBRANDT, JEFFREY D

APPLICANT: KOTZBAUER, PAUL T

APPLICANT: LAMPE, PATRICIA A

APPLICANT: KLEIN, ROBERT

APPLICANT: DESAUVAGE, FRED

TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAFERKAMP, L.C.

STREET: 7733 FORSYTH BOULEVARD, SUITE 1400

CITY: ST. LOUIS

STATE: MO

COUNTRY: USA

ZIP: 63105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-931-858E-201

Query Match 61.4%; Score 289.4; DB 4; Length 291;
Best Local Similarity 99.7%; Pred. No. 1.5e-52;
Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 181 GCCCTGTGTCATGCCAGCTGTGGAGCCTGACCCCTGTCCGTGGCAGAGCTAGGCGCTG 240
Db 1 GCCCTGTGTCATGCCAGCTGTGGAGCCTGACCCCTGTCCGTGGCAGAGCTAGGCGCTG 60
QY 241 GGCTACGCCTCAGAGGAGAGGTTCATCTCCGCTACTGCGCGGCGAGCTGCCCGTGGT 300
Db 61 GGCTACGCCTCAGAGGAGAGGTTCATCTCCGCTACTGCGCGGCGAGCTGCCCGTGGT 120
QY 301 GCCCGACCCAGCATGGCCTGGCGCTGCGCGGCTGACGGCGAGCGGCGGAGCCACGGT 360
Db 121 GCCCGACCCAGCATGGCCTGGCGCTGCGCGGCTGACGGCGAGCGGCGGAGCCACGGC 180
QY 361 GGGCCCTGCTGCGCGGCCACTCGCTACACCGAGCTGGCCTTCTCGATGATGCCGACCGC 420
Db 181 GGGCCCTGCTGCGCGGCCACTCGCTACACCGAGCTGGCCTTCTCGATGATGCCGACCGC 240
QY 421 TGGCAGCGGCTGCCCGAGCTCTCGCGGCTGCTCGGCGCTGTGGTGGCTGA 471
Db 241 TGGCAGCGGCTGCCCGAGCTCTCGCGGCTGCTCGGCGCTGTGGTGGCTGA 291

RESULT 8
US-08-931-858E-202/c
Sequence 202, Application US/08931858E
Patent No. 622022
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-931-858E-202

Query Match 61.4%; Score 289.4; DB 4; Length 291;
Best Local Similarity 99.7%; Pred. No. 1.5e-52;
Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 181 GCCCTGTGTCATGCCAGCTGTGGAGCCTGACCCCTGTCCGTGGCAGAGCTAGGCGCTG 240
Db 291 GCCCTGTGTCATGCCAGCTGTGGAGCCTGACCCCTGTCCGTGGCAGAGCTAGGCGCTG 232
QY 241 GGCTACGCCTCAGAGGAGAGGTTCATCTCCGCTACTGCGCGGCGAGCTGCCCGTGGT 300
Db 231 GGCTACGCCTCAGAGGAGAGGTTCATCTCCGCTACTGCGCGGCGAGCTGCCCGTGGT 172
QY 301 GCCCGACCCAGCATGGCCTGGCGCTGCGCGGCTGACGGCGAGCGGCGGAGCCACGGT 360
Db 171 GCCCGACCCAGCATGGCCTGGCGCTGCGCGGCTGACGGCGAGCGGCGGAGCCACGGC 112
QY 361 GGGCCCTGCTGCGCGGCCACTCGCTACACCGAGCTGGCCTTCTCGATGATGCCGACCGC 420
Db 111 GGGCCCTGCTGCGCGGCCACTCGCTACACCGAGCTGGCCTTCTCGATGATGCCGACCGC 52
QY 421 TGGCAGCGGCTGCCCGAGCTCTCGCGGCTGCTCGGCGCTGTGGTGGCTGA 471
Db 51 TGGCAGCGGCTGCCCGAGCTCTCGCGGCTGCTCGGCGCTGTGGTGGCTGA 1

RESULT 9
US-08-931-858E-222
Sequence 222, Application US/08931858E
Patent No. 622022
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

Query Match 53.1%; Score 250; DB 4; Length 471;
Best Local Similarity 73.4%; Pred. No. 2.7e-44;
Matches 348: Conservative 0; Mismatches 120; Indels 6; Gaps 2;

		matches	546:	Conservative	0:	Mismatches	140:	Indels	0:	Gaps
QY	1	ATGGCCGTGAGGAAGTTCTCGTGGGCTCTCTGCTGCCTCTGTCCCTCAGCTGGGACAG	60							
Db	1	ATGGCTGCAGGAAGACTTCGGATCCTGTCTGCTGCTCTCTGTCTGTCACACCAGGCCCTC	60							
QY	61	GGCTGGGGCCCCCATGCCCCTGGGGTTCGCCGTGGCCGATGGAGAGTTCCTGTCTGTAACAG	120							
Db	61	GGCTGGGTCTTGATCTTCAAGAGCTTCTGTGGCAGATA---AGCTCTATTTTGGCAAG	117							
QY	121	GTGGCAAAAGCTGGAGGAGCCTGGCTGGGGACCCACCG---CCGCCTTGCCCGCTCGCG	177							
Db	118	ATGGCAGAGACTAGAGGAGCTGGACGCCCATCAGGCTAACAACCATGTCCGCTCTTCCA	177							
QY	178	CGAGCCCTGTCTGCTCCATGCCAGCTGTGGAGCCTGACCCCTGTCCGTGGCAGAGCTTAGGC	237							
Db	178	AGAGCTTGGCTGTTCTNCGCGACTGTGGAGCCTGACCCTAGCCCTGGCTGAGCTGGGC	237							
QY	238	CTGGGCTACGGCTCAGAGGAGAAGTCACTTTCGGGTACTTGGCGGGCAGCTGCCCCCGT	297							
Db	238	CTGGGCTATGCTCTCGSAGSAGAAGTCACTTTCGGATACTGTGTGGCAGCTGTGCCCAA	297							
QY	298	GGTGC CCGCACCCACAGTATGCGCTTGGCGCTGGCCCGGCTGCAGGGCCAGAGGCCGAGCCAC	357							
Db	298	GAGGCCGTATACCCAGCACAGTCTGGTACTTGGCCCGGCTTCGAGGGCGGGGTCGAGGCCAT	357							
QY	358	GSTGGGCCCTGCTCGCGGCCACTCCGCTACACGAGGTGGCTTTCCTCGATGACCGGCCAC	417							
Db	358	GGCCGACCCTCTGCCAACCCCACTATGCTGATGTGACCTTCTTCTTGATGATCAGCAC	417							
QY	418	CCTGGCAGCGGCTGCCCCACAGCTCTCGGGGGCTGCTCGCGCTGTGGTGGGTGA	471							
Db	418	CATTGGCAGAGCTTGCTCACTCAGCTCCTCAGCTGCAGCTTGTGGCTGTGGTGGCTGA	471							

```

RESULT 11
US-8-931-858E-180/c
Sequence 180, Application US/08931858E
Patent No. 6222022
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSPEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFFERKAMP, I.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
Zip: 63105

```


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Result No.	Score	Query %		Length	DB ID	Description
		Match				
1	471	100.0	471	20	AA650507	Human pre-pro pers
2	467.8	99.3	471	20	AA650509	WO9914235 Seq ID N
3	376	79.8	556	21	AA250334	Human Persephin-AR
4	376	79.8	556	21	AA250337	Human Persephin-AR
5	343.4	72.9	974	24	ABQ54526	Human ovarian anti
6	343	72.8	974	22	AA657993	Human secreted pro
7	332.4	70.6	973	22	AA657995	Human secreted pro
8	291.6	61.9	1173	23	AA681308	DNA encoding novel
9	291	61.8	291	20	AA650503	Human persephin pr

QY 396 GGCCTTCTCGATGACGGCAGCGCTGGCAGCGGCTGCCAGCTCTCGCGGGCTGCTG 455
 DB 481 GGCCTTCTCGATGACGGCAGCGCTGGCAGCGGCTGCCAGCTCTCGCGGGCTGCTG 540
 QY 456 CGGCTGTGGTGGCTGA 471
 DB 541 CGGCTGTGGTGGCTGA 556

RESULT 4
 AAZ50337/c
 ID AAZ50337 standard; DNA: 556 BP.
 XX
 AC AAZ50337;
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE Human Persephin-ARF complementary DNA.
 XX
 KW Persephin-ARF; alternative reading frame; ARF; cell proliferation;
 KW differentiation; nootropic; neuroprotective; analgesic; haemostatic;
 KW antiparkinsonian; anticonvulsant; antianaemic; immune stimulating;
 KW immunosuppressive; antiallergic; activin; inhibin; antifertility;
 KW chemotactic; chemokinetic; anti-inflammatory; antibacterial; cytostatic;
 KW antiarthritic; thrombolytic; treatment; neuropathy; Huntington's;
 KW amyotrophic lateral sclerosis; Alzheimer's; Parkinson's; brain injury;
 KW Shy-Drager syndrome; stroke; tumour; multiple sclerosis; leucopaenia;
 KW diabetes; anaemia; thrombocytopaenia; immune deficiency; Crohn's disease;
 KW infection; autoimmune disorder; allergy; infertility; septic shock;
 KW arthritis; nephritis; inflammatory bowel disease; anaphylaxis;
 KW haemophilia; thrombosis; gene therapy; human; complement; ds.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..487
 FT /*tag= a
 FT /note= "This region is specifically claimed"

WO200006731-A2.
 XX
 PN 10-FEB-2000.
 XX
 PD 30-JUL-1999; 99WO-US17277.
 XX
 PF 31-JUL-1998; 98US-0126799.
 XX
 PR (UNITW) UNIV WASHINGTON.
 PA (GETH) GENENTECH INC.
 XX
 PI Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA, Klein R;
 DE De Sauvage F;
 XX
 DR WPI; 2000-183126/16.
 XX
 XX Novel protein designated persephin-ARF, used for treating, e.g.
 PT amyotrophic lateral sclerosis and Alzheimer's disease -
 XX
 PS Claim 14; Page 39-40; 45pp; English.
 XX
 CC The present sequence is the human persephin-ARF complementary DNA.
 CC Persephin-ARF DNA in its alternative reading frame (ARF)
 CC encodes human persephin-ARF. Persephin-ARF has cell
 CC proliferation, differentiation, nootropic, neuroprotective, analgesic,
 CC antiparkinsonian, anticonvulsant, antianaemic, haemostatic,
 CC immune stimulating, immunosuppressive, antiallergic, activin, inhibin,
 CC antifertility, chemotactic, chemokinetic, anti-inflammatory,
 CC antibacterial, antarthritic, thrombolytic and cytostatic activity.
 CC It can be used to treat conditions associated with altered expression
 CC of persephin-ARF like neuropathy, amyotrophic lateral sclerosis,
 CC Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC Shy-Drager syndrome, stroke, brain injury, tumours, multiple sclerosis,
 CC diabetes, anaemia, thrombocytopaenia, leucopaenia, immune deficiencies,

CC Infections, autoimmune disorders, allergy, infertility, septic shock,
 CC arthritis, nephritis, inflammatory bowel disease, Crohn's disease,
 CC anaphylaxis, haemophilia and thrombosis. Persephin-ARF DNA can be used
 CC in gene therapy.
 XX
 SQ Sequence 556 BP; 101 A; 179 C; 207 G; 69 T; 0 other;
 Query Match 79.8%; Score 376; DB 21; Length 556;
 Best Local Similarity 84.7%; Pred. No. 3.5e-67;
 Matches 471; Conservative 0; Mismatches 0; Indels 85; Gaps 1;
 QY 1 ATGGCCCTAGGGAAGTTCTCTGCTGGGCTCTCTGCTGCTCTCTGCTGAGCTGGGACAG 60
 DB 556 ATGGCCCTAGGGAAGTTCTCTGCTGGGCTCTCTGCTGCTCTCTGCTGAGCTGGGACAG 497
 QY 61 GGCTGGGGCCCCGATGCCGTGGGGTTCCCGTGGCCGATGAGAGTTCTGCTCTGAACAG 120
 DB 496 GGCTGGGGCCCCGATGCCGTGGGGTTCCCGTGGCCGATGAGAGTTCTGCTCTGAACAG 437
 QY 121 GTGGCAAGGCTGGAGGGACCTGGGCTG----- 147
 DB 436 GTGGCAAGGCTGGAGGGACCTGGGCTGGGTAAGGACTTCCAGGGACCTCTGTGACTTCC 377
 QY 148 -----GGCACCCA 155
 DB 376 CAACTTCCCGCCGCTGACCTGCTCACTGTCAGGGCCCTTCCCTCCACAGGACCCA 317
 QY 156 CCGCCCTTGGCCGCTGCGCGAGCCCTGTCTGGTCCATGCCAGCTGTGGAGCCTGAC 215
 DB 316 CCGCCCTTGGCCGCTGCGCGAGCCCTGTCTGGTCCATGCCAGCTGTGGAGCCTGAC 257
 QY 216 CCTGCTCGCTGGCAGAGCTAGGCTGGGCTACGCCCTACAGAGGAGAGTTCATCTTCCGCTA 275
 DB 256 CCTGCTCGCTGGCAGAGCTAGGCTGGGCTACGCCCTACAGAGGAGAGTTCATCTTCCGCTA 197
 QY 276 CTGGCCCGGCGAGCTGCCCCGGTGGTGGTGGCCGACCCAGCATGGCTGGCGTGGCGGCT 335
 DB 196 CTGGCCCGGCGAGCTGCCCCGGTGGTGGTGGCCGACCCAGCATGGCTGGCGTGGCGGCT 137
 QY 336 GCAGGGCCAGGGCGGCGAGCCACGGTGGGCTGTGTCGCGGCCCTACTGCTACACCGAGCT 395
 DB 136 GCAGGGCCAGGGCGGCGAGCCACGGTGGGCTGTGTCGCGGCCCTACTGCTACACCGAGCT 77
 QY 396 GGCTTCTCTGATGACCGCCAGCGCTGGCAGCGGCTGCCAGCTCTCGGGGGCTGCTG 455
 DB 76 GGCTTCTCTGATGACCGCCAGCGCTGGCAGCGGCTGCCAGCTCTCGGGGGCTGCTG 17
 QY 456 CGGCTGTGGTGGCTGA 471
 DB 16 CGGCTGTGGTGGCTGA 1

RESULT 5
 ABQ54526
 ID ABQ54526 standard; cDNA: 974 BP.
 XX
 AC ABQ54526;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HSKNP59 cDNA, SEQ ID NO:406.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; gene; ss.
 XX

Qy 162 CCTTGCCCGCTGGCCGAGCCCTGTCTGGTCCATGCGAGCTGTGGAGCCTGACCCCTGTC 221
Db 120 CCATGTCCGTCTTCCAAGAGCCTTGGCTGGTTCATGCCGACTGTGGAGCCTGACCCCTACC 179
Qy 222 CGTGGCAGAGCTAGGCTAGCGCTACGCCCTCAGAGGAGAAGGTATCTTCGGTACTGCGC 281
Db 180 AGTGGCTGAGCTGGGCTGGGCTATGCCCTCGGAGGAGAGGTATCTTCGATACTGTGC 239
Qy 282 CGGAGCTGGCCCGCTGGTGGCCGACCCAGCATGGGCTGGCGCTGGCCCGGCTGCAGGG 341
Db 240 TGGCAGCTGTCCCAAGAGGCCCGTACCCAGCAGCATGTGGTACTGGCCCGGCTTCGAGG 299
Qy 342 CCAGGGCCGAGCCACAGGTGGGCCCTGTGCGGCCCCACTCGCTACACCCAGCCTGGCCTT 401
Db 300 GCGGGTTCGAGCCCATGGCCGACCTGTGCCAGCCACCAGCTATGCTGATGTGACCTT 359
Qy 402 CCTCGATGACCCGACCGCTGGCAGGGGCTGCCCGAGCTCTCGGGGCTGCCTGGCGCTG 461
Db 360 CCTGATGATCAGACCATTTGGCAGAGCTGCTCAGCTCTCAGCTGCAGCTTGTGGCTG 419
Qy 462 TGGTGGCTGA 471
Db 420 TGGTGGCTGA 429

Search completed: March 7, 2003, 11:44:13
Job time : 316 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2003, 11:36:19 ; Search time 2458 Seconds
(without alignments)
3103.366 Million cell updates/sec

Title: US-09-220-617B-203

Perfect score: 471
Sequence: 1 ATGGCCCTAGGAAGTCTCT.....CCTGGCGCTGTGGTGGTGA 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	322.4	68.5	510	14	BM987233
C 2	83.2	17.7	518	10	AW050617
C 3	79.8	16.9	643	13	BM65236
C 4	79.8	16.9	722	14	BM677930
5	79.8	16.9	753	14	BQ189286
6	78.8	16.7	839	17	CNS01VCA

7	69.2	14.7	1544	11	AK015393
8	68.4	14.5	1025	17	CNS022JX
9	67.2	14.3	439	10	AW611702
10	66.4	14.1	670	10	BB641881
11	66.2	14.1	514	9	AI768514
12	63.4	13.5	925	17	CNS0091P
13	62.8	13.3	932	17	CNS0072Q
14	62.4	13.2	932	17	CNS0072Q
15	61.8	13.1	604	14	BM725812
16	61.6	13.0	1080	14	BM726983
17	61	13.0	1080	14	CNS04PM4
18	60.8	12.9	522	12	BF416337
19	60.4	12.8	471	12	BF376439
20	60.4	12.8	489	12	BF407806
21	60	12.7	464	14	BM999804
22	60	12.7	546	14	BO209765
23	59.6	12.7	925	17	CNS0091P
24	58	12.3	839	17	CNS004NB
25	57.8	12.3	670	10	BB547879
26	57.4	12.2	693	14	BQ192856
27	57.2	12.1	679	14	BM702521
28	57.2	12.1	1203	17	CNS015Y4
29	54.8	11.6	350	9	AI598581
30	54.6	11.6	365	9	AI548543
31	54.6	11.6	1160	11	AK002508
32	54.2	11.5	854	13	BI407479
33	53.6	11.4	1538	17	AG030607
34	53.2	11.3	813	17	AZ193936
35	53.2	11.3	938	17	AG130978
36	52.4	11.1	935	17	CNS006XK
37	52.4	11.1	935	17	CNS006XK
38	52.4	11.1	1101	17	CNS017SY
39	52.2	11.1	776	17	CNS010RY
40	51.6	11.0	1009	17	CNS010EW
41	51.4	10.9	704	17	AG060135
42	51.4	10.9	960	17	AG036217
43	51.4	10.9	1128	14	BQ710735
44	51.2	10.9	1040	12	BG786331
45	51.2	10.9	1244	12	BG646745

ALIGNMENTS

RESULT 1
BM987233/c
LOCUS BM987233 510 bp mRNA linear EST 25-MAR-2002
DEFINITION UI-H-CO0-aql-e-08-0-UI.sl NCI-CGAP-Sub9 Homo sapiens cDNA clone
IMAGE: 3104342 3', mRNA sequence.
ACCESSION BM987233
VERSION BM987233.1 GI:19706622
KEYWORDS EST.
SOURCE Human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 510)
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLYA-Yes.
FEATURES Location/Qualifiers
source 1..510

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3104342"
/clone_lib="NCI CGAP_Sub9"
/tissue_type="mixed"
/dev_stage="mixed"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: p773-Pac (Pharmacia) with a modified
polylinker; Site.1: EcoR I; Site.2: Not I; tissues:
Cholonic mucosa with Crohns disease, Cholonic mucosa with
ulcerative colitis, Fetal thymus, Cervix, Cervical
adenosquamous carcinoma, Ligament cells, Prostate
carcinoma, Bladder carcinoma, Brain oligodendrocyte ;
NCI CGAP Sub9 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are CGTC, AACG, GGCG,
GGAG, TAGC, TAGC, ATGG, AGACA, ATCAC. For additional
information, contact: Bento Soares, bento@soaresulowa.edu
TAG_Lib=UI-H-00
TAG_TISSUE=colonic mucosa with Crohns disease
TAG_SEQ=CGTC"

BASE COUNT      78 a  165 c  178 g   89 t
ORIGIN

Query Match      68.5%; Score 322.4; DB 14; Length 510;
Best Local Similarity 99.7%; Pred. No. 2.3e-55;
Matches 323; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  148 GGCACCCACCGCCCTGTCGCGCCGAGCCCTGTCTGTGTCATGCCAGCTGTGG 207
DB  488 GGCACCCACCGCCCTGTCGCGCCGAGCCCTGTCTGTGTCATGCCAGCTGTGG 429
QY  208 AGCTGTACCTGTCCGTGGCAGAGCTAGGCTGGGCTAGGCTCAGAGAGAGTGCATC 267
DB  428 AGCTGTACCTGTCCGTGGCAGAGCTAGGCTGGGCTAGGCTCAGAGAGAGTGCATC 369
QY  268 TTCGCTACTGCGCGGCGAGCTGCCCCCGTGTGTCGCGCCAGCATGGCGCTG 327
DB  368 TTCGCTACTGCGCGGCGAGCTGCCCCCGTGTGTCGCGCCAGCATGGCGCTG 309
QY  328 GCGCGGCTGACGGGCGGCGAGCCGACGCTGGGCGCCCTGTGTCGCGCCGACCTCGGTAC 387
DB  308 GCGCGGCTGACGGGCGGCGAGCCGAGCCGCGCGGCGCCCTGTGTCGCGCCGACCTCGGTAC 249
QY  388 ACCGAGTGGCTTCTTCGATGACCGCCAGCCGCTGCGAGCGCTGCCCGACCTCGCGCG 447
DB  248 ACCGAGTGGCTTCTTCGATGACCGCCAGCCGCTGCGAGCGCTGCCCGACCTCGCGCG 189
QY  448 GCTGCTGCGGCTGTGTGGCTGA 471
DB  188 GCTGCTGCGGCTGTGTGGCTGA 165
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```
RESULT 2
AW050617/c      AW050617      518 bp      mRNA      linear      EST 09-MAR-2000
LOCUS          wz19d01.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone
DEFINITION      IMAGE:2558497 3' similar to SW:NRFTN_HUMAN Q99748 NEURTURIN
PRECURSOR. 1, mRNA sequence.
ACCESSION      AW050617
VERSION        AW050617.1 GI:5912887
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
1 (bases 1 to 518)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               This clone is available royalty-free through LILNL; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               Insert length: 1016 Std Error: 0.00
               Seq primer: -400P from Gibco
               High quality sequence stop: 376.
               Location/Qualifiers
FEATURES
source
1..518
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2558497"
/clone_lib="Soares_dieckgraefe_colon_NHCD"
/tissue_type="colonic mucosa from 3 patients with Crohn's
disease"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: colon; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGCTCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Tissue samples
provided by Dr. Brian Dieckgraefe (Washington University,
dieck@im.wustl.edu); colonic mucosa represents a range of
disease involvement from moderate to severe Crohn's
disease; samples include both perforating (fistulas) and
non-perforating samples. Library constructed by Bento
Soares and M. Fatima Bonaldo.

BASE COUNT      67 a  198 c  187 g   62 t   4 others
ORIGIN

Query Match      17.7%; Score 83.2; DB 10; Length 518;
Best Local Similarity 58.2%; Pred. No. 3.2e-07;
Matches 189; Conservative 0; Mismatches 121; Indels 15; Gaps 2;

QY  154 CACCGCGCCCTTCCCGCGCTGCGCGAGCCCTGTCTGTGTCATGCCAGCTGTGAGCGCTG 213
DB  482 CCCGCGCGCGCGCGCGCTGCGCGCTTGGGGCGCGGCTTTCGGGCTCGCGAGCTG 423
QY  214 ACCCTGTCTCGTCGACAGCTAGGCTGGGCTACGCCCTCAGAGAGAGAGTCTTCCGC 273
DB  422 AAGTGTGCGCTGAGCGAGCTGGGCGCTTACGGCTCCGACGAGAGCGTGTCTTCCGC 363
QY  274 TACTGCGCGCGCGAGCTGCCCGCTGTGTCGCGCGACCC-----CAGCATGGCGCTG 321
DB  362 TACTGCGCGCGCGCTCGGAGGCTGCGCGCGCGCTACGACCTCGGCTCGGACCACTG 303
QY  322 CGCGTGGCGCGGCTCAGGGCCAGGGCCAGCGTGGGCGCTGCTGGCGGCCACT 381
DB  302 CGGCGCGCGCGCGCTCGGCGCGGAGCGGGTGGCGCGCGAGCGCTGCTGGCGGCCAGC 243
QY  382 CGCTAC---ACCGACGTGGCGCTTCCTCGATGACCGCCCGCGCGCTGGCGCGCGCTG 438
DB  242 GCCTACGAGGACGAGGTGCTCTCTCTGGAGCGCGACAGCGCGCTACCGAGGTGCAGG 183
QY  439 CTCTCGCGCGCTGCTCGCGCTGTG 463
DB  182 CTGTCGCGCGCGGAGTGCCTGCGCTGCG 158

RESULT 3
BM665236/c      BM665236      643 bp      mRNA      linear      EST 27-FEB-2002
LOCUS          UI-E-CL1-afg-1-03-0-UI.s1 UI-E-CL1 Homo sapiens cDNA clone
DEFINITION      UI-E-CL1-afg-1-03-0-UI 3', mRNA sequence.
ACCESSION      BM665236
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2003, 11:33:49 ; Search time 2567 Seconds
(without alignments)
5339.860 Million cell updates/sec

Title: US-09-220-617B-203
Perfect score: 471
Sequence: 1 ATGGCCGTAGGAAGTTCCT.....CCTGGCGGTGGGGCTGA 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: gb_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_or.*
21: em_ov.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pin.*
35: em_htg_rod.*
36: em_htg_man.*
37: em_htg_vit.*
38: em_sy.*
39: em_htg_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	471	100.0	471	9	AF040962	AF040962 Homo sapi
2	372.8	79.2	2180	9	AK055490	AK055490 Homo sapi
3	372.8	79.2	118819	9	AC011491	AC011491 Homo sapi
4	250	53.1	471	10	AF040960	AF040960 Mus muscu
5	250	53.1	471	10	AF040961	AF040961 Rattus no
6	207.6	44.1	405	6	AR152134	AR152134 Sequence
7	207.6	44.1	544	6	AR152107	AR152107 Sequence
8	207.6	44.1	559	6	AR152120	AR152120 Sequence
9	206	43.7	213137	10	AC073683	AC073683 Mus muscu
10	203	43.1	559	6	AR152121	AR152121 Sequence
11	203	43.1	142758	2	AC129629	AC129629 Rattus no
12	199.8	42.4	291	6	AR152133	AR152133 Sequence
13	195	41.4	291	6	AR152135	AR152135 Sequence
14	189.6	40.3	391	6	AR152109	AR152109 Sequence
15	186.6	39.6	273	6	AR152100	AR152100 Sequence
16	180.6	38.3	267	6	AR152098	AR152098 Sequence
17	180.6	38.3	267	6	AR152099	AR152099 Sequence
18	148.8	31.6	336	6	AR152104	AR152104 Sequence
19	148.8	31.6	336	6	AR152108	AR152108 Sequence
20	79.8	16.9	306	6	AR001492	AR001492 Sequence
21	79.8	16.9	306	6	AR005228	AR005228 Sequence
22	79.8	16.9	306	6	AR044780	AR044780 Sequence
23	79.8	16.9	306	6	AR062986	AR062986 Sequence
24	79.8	16.9	306	6	AR152050	AR152050 Sequence
25	79.8	16.9	425	6	AR001505	AR001505 Sequence
26	79.8	16.9	425	6	AR005241	AR005241 Sequence
27	79.8	16.9	425	6	AR044793	AR044793 Sequence
28	79.8	16.9	425	6	AR062999	AR062999 Sequence
29	79.8	16.9	425	6	AR152063	AR152063 Sequence
30	79.8	16.9	591	6	AR001494	AR001494 Sequence
31	79.8	16.9	591	6	AR005230	AR005230 Sequence
32	79.8	16.9	591	6	AR044782	AR044782 Sequence
33	79.8	16.9	591	6	AR062988	AR062988 Sequence
34	79.8	16.9	594	6	AR152052	AR152052 Sequence
35	79.8	16.9	594	9	HSU78110	U78110 Human prepr
36	79.8	16.9	1160	9	HSU802618	AL161995 Homo sapi
37	79.8	16.9	80893	9	AC024592	AC024592 Homo sapi
38	79.8	16.9	187488	2	AC010454	AC010454 Homo sapi
39	78.2	16.6	169893	2	AC021165	AC021165 Homo sapi
40	69.2	14.7	675	6	AX470388	AX470388 Sequence
41	69.2	14.7	675	10	AF109402	AF109402 Mus muscu
42	69.2	14.7	190446	2	AL627128	AL627128 Mus muscu
43	69.2	14.7	195804	2	AL611952	AL611952 Mus muscu
44	67.2	14.3	663	6	AX055740	AX055740 Sequence
45	67.2	14.3	663	6	AX201382	AX201382 Sequence

ALIGNMENTS

RESULT 1
AF040962
LOCUS AF040962
DEFINITION Homo sapiens persepchin mRNA, complete cds.
ACCESSION AF040962
VERSION AF040962.1 GI:2935709
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 471)
Leitner,M.L., Tansey,M.G., Lampe,P.A., Heuckeroth,R.O.,
Kotzbauer,P.T., Simburger,K.S., Golden,J.P., Davies,J.A.,
Fahner,T.J., de Sauvage,F.,
PRI 06-MAR-1998

QY	216	CTGTGCGTGGCAGAGCTAGGCGCTGGGGTACGCGCTCAGAGAGAAGGTCACTTCCGCGTA	275
DB	1779	CCTGTCCGTGGCAGAGCTAGGCGCTGGGGTACGCGCTCAGAGAGAAGGTCACTTCCGCGTA	1838
QY	276	CTGCGCCGGCAGCTGCCCCCGGTGGTGTCGCCGACCCAGCATGGCGCTGGCCCGCGCT	335
DB	1839	CTGCGCCGGCAGCTGCCCCCGGTGGTGTCGCCACCCAGCATGGCGCTGGCCCGCGCT	1898

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Best Local Similarity 84.4%; Pred. No. 5.5e-55;
Matches 469; Conservative 0; Mismatches 2; Indels 85; Gaps 1;

QY 1 ATGCGCGTAGGAAAGTTCTGCTGGGCTTCTGCTGCTCCTGCGAGCTGGGACAG 60
Db 77366 ATGCGCGTAGGAAAGTTCTGCTGGGCTCCCTGCTGCTCCTGCGAGCTGGGACAG 77307

QY 61 GGCTGGGGCCCCGATGCGCCGCTGGGGTTCCCGTGGCCCATGAGAGATTCTCGTCTGAACAG 120
Db 77306 GGCTGGGGCCCCGATGCGCCGCTGGGGTTCCCGTGGCCCATGAGAGATTCTCGTCTGAACAG 77247

QY 121 GTGGCAAGGCTGGAGGACCTGGCGTG----- 147
Db 77246 GTGGCAAGGCTGGAGGACCTGGCGTG----- 17187

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Qy 148 -----GGCACCCA 155

Db 77126 CCGCCCCCTTGCCCCGCCCTGCCGCCGAGCCCTGTCTGGTCCCATGCCAGCTGTGGAGTTGAC 77067

Db 77066 CCTGTCCTGGCAGAGCTAGGCCTGGGCTACGCCCTCAGAGGAGAGGTCATCTTCCGCTA 77007

Db 77006 CTGCGCCGGCAGCTGCCCCCGTGGTGCCCGCACCCAGCATGGCCTGGCGCTGGCCCGGCT 76947

Db 76946 GCAGGGCCAGGGCCGAGCCACGGGGGCCCTGCTGCCGGCCCACTCGCTACACGACGT 76887

Db 76886 GGCCTTCCTCGATGACCCGCCACCGCTGGCAGCGGCTGCCCCAGCTCTCGGCGGCTGCCCTG 76827

A

LOCUS	AF040960	471 bp	mRNA	linear	ROD 06-MAR-1998
DEFINITION	Mus musculus perisperm mRNA complete cds				

VERSION
KEYWORDS
AF040960.1 GI:2935705

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS
Milbrandt, J., de Sauvage, F. J., Fahrner, T. J., Balch, R. H.,
Leitner, M. L., Tansey, M. G., Lampe, P. A., Heuckeroth, R. O.

Vejsada, R., Kato, A.C., Hynes, M., Sherman, D., Nishimura, M., Wang, L.-C., Vandlen, P., Moffett, B., and Hynes, M.

TITLE Persephin, a novel neurotrophic factor related to GDNF and

MEDLINE 98150950

REFERENCE 2 (pages 1 to 4/1)

AUTHORS Fahrner, T. J., Heuckeroth, R. O., Simburger, K. S., Kotzbauer, P. T. and

Submitted (15 JAN 1996) RADIOLOGY, WASHINGTON UNIVERSITY MEDICAL SCHOOL, 660 S. Euclid Ave., St. Louis, MO 63110, USA


```

REFERENCE 1 (bases 1 to 405)
AUTHORS Johnson,E.M. Jr., Milbrandt,J.D., Kotzbauer,P.T. and Lampe,P.A.
TITLE Persephin and related growth factors
JOURNAL Patent: US 6232449-A 175 15-MAY-2001;
FEATURES Location/Qualifiers
source 1..405
BASE COUNT 71 a 132 c 108 g 94 t
ORIGIN

Query Match 44.1%; Score 207.6; DB 6; Length 405;
Best Local Similarity 79.4%; Pred. No. 3.5e-26;
Matches 246; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 162 CTTTCCCGCTGCGCCGAGCCCTGTCTGTCATGCCAGCTGTGGAGCTGACCCCTGTC 221
DB 96 CCATGTCGCTTCCAGAGCCCTTGGCTGTTTCATGCCAGCTGTGGAGCTGACCCCTACC 155
QY 222 CTTGCGAGAGCTAGCCCTGGCTAGCCCTCAGAGGAGAGGTCTATCTTCCGCTACTGCGC 281
DB 156 AGTGCTGAGCTGGCCCTGGCTATGCCCTCGGAGGAGAGGTCTATCTTCCGATACTGTC 215
QY 282 CGGAGCTGCCCGCTGTGTGCCCGACCCAGCATGGCTGGCGCTGGCCCGGCTGCAGGG 341
DB 216 TGGCAGCTGTCCCAAGAGGCCCGTACCAGCACAGCTGTGTACTGGCCCGCTTCGAGG 275
QY 342 CCAGGGCGAGCCACGGTGGCCCTGCTGCGGGCCACTCGCTACACCGAGCTGGCCCTT 401
DB 276 GCGGGGTGAGCCCTAGCCCTGGCCGAGCCCTGCTGCCAGCCACAGCTATGCTGATGACCTT 335
QY 402 CTTGATGACCGCCACCGCTGGCAGCGGCTGCCCGAGCTCTCGGCGGCTGCTGGCGGTG 461
DB 336 CTTGATGATCAGCACCATTGGCAGCAGCTGCTCAGCTCTCAGCTGAGCTTGTGGCTG 395
QY 462 TGGTGGCTGA 471
DB 396 TGGTGGCTGA 405

RESULT 7
AR152107 544 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 105 from patent US 6232449.
DEFINITION AR152107
ACCESSION AR152107
VERSION AR152107.1 GI:15118157
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 544)
AUTHORS Johnson,E.M. Jr., Milbrandt,J.D., Kotzbauer,P.T. and Lampe,P.A.
TITLE Persephin and related growth factors
JOURNAL Patent: US 6232449-A 105 15-MAY-2001;
FEATURES Location/Qualifiers
source 1..544
BASE COUNT 115 a 158 c 153 g 118 t
ORIGIN

Query Match 44.1%; Score 207.6; DB 6; Length 544;
Best Local Similarity 79.4%; Pred. No. 3.5e-26;
Matches 246; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 162 CTTTCCCGCTGCGCCGAGCCCTGTCTGTCATGCCAGCTGTGGAGCTGACCCCTGTC 221
DB 120 CCATGTCGCTTCCAGAGCCCTTGGCTGTTTCATGCCAGCTGTGGAGCTGACCCCTACC 179
QY 222 CTTGCGAGAGCTAGCCCTGGCTAGCCCTCAGAGGAGAGGTCTATCTTCCGCTACTGCGC 281
DB 180 AGTGCTGAGCTGGCCCTGGCTATGCCCTCGGAGGAGAGGTCTATCTTCCGATACTGTC 239
QY 282 CGGAGCTGCCCGCTGTGTGCCCGACCCAGCATGGCTGGCGCTGGCCCGGCTGCAGGG 341

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DB 240 TGGCAGCTGTCCCAAGAGGCCCGTACCAGCACAGCTGTGGTACTGCGCCGCTTCGAGG 299
QY 342 CCAGGGCGAGCCACGGTGGCCCTGCTGCGGGCCCACTCGCTACACCGAGCTGGCCCTT 401
DB 300 GCGGGGTGAGCCCATGGCCAGCCCTTCTGCCAGCCACACGATGCTGTGATGTGACCTT 359
QY 402 CTTGATGATCAGCACCATTGGCAGCAGCTGCTCAGCTGCTCAGCTGCGAGCTTGTGGCTG 461
DB 360 CTTGATGATCAGCACCATTGGCAGCAGCTGCTCAGCTGCTCAGCTGCGAGCTTGTGGCTG 419
QY 462 TGGTGGCTGA 471
DB 420 TGGTGGCTGA 429

RESULT 8
AR152120 559 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 131 from patent US 6232449.
DEFINITION AR152120
ACCESSION AR152120
VERSION AR152120.1 GI:15118170
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 559)
AUTHORS Johnson,E.M. Jr., Milbrandt,J.D., Kotzbauer,P.T. and Lampe,P.A.
TITLE Persephin and related growth factors
JOURNAL Patent: US 6232449-A 131 15-MAY-2001;
FEATURES Location/Qualifiers
source 1..559
BASE COUNT 100 a 173 c 155 g 131 t
ORIGIN

Query Match 44.1%; Score 207.6; DB 6; Length 559;
Best Local Similarity 79.4%; Pred. No. 3.5e-26;
Matches 246; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 162 CTTTCCCGCTGCGCCGAGCCCTGTCTGTCATGCCAGCTGTGGAGCTGACCCCTGTC 221
DB 250 CCATGTCGCTTCCAGAGCCCTTGGCTGTTTCATGCCAGCTGTGGAGCTGACCCCTACC 309
QY 222 CTTGCGAGAGCTAGCCCTGGCTAGCCCTCAGAGGAGAGGTCTATCTTCCGCTACTGCGC 281
DB 310 AGTGCTGAGCTGGCCCTGGCTATGCCCTCGGAGGAGAGGTCTATCTTCCGATACTGTC 369
QY 282 CGGAGCTGCCCGCTGTGTGCCCGACCCAGCATGGCTGGCGCTGGCCCGGCTGCAGGG 341
DB 370 TGGCAGCTGTCCCAAGAGGCCCGTACCAGCACAGCTGTGGTACTGCGCCGCTTCGAGG 429
QY 342 CCAGGGCGAGCCACGGTGGCCCTGCTGCGGGCCCACTCGCTACACCGAGCTGGCCCTT 401
DB 430 GCGGGGTGAGCCCATGGCCGACCCCTGCTGCCAGCCACACGCTATGCTGTGATGTGACCTT 489
QY 402 CTTGATGATCAGCACCATTGGCAGGAGCTGCTCAGCTGCTCAGCTGCGAGCTTGTGGCTG 461
DB 490 CTTGATGATCAGCACCATTGGCAGGAGCTGCTCAGCTGCTCAGCTGCGAGCTTGTGGCTG 549
QY 462 TGGTGGCTGA 471
DB 550 TGGTGGCTGA 559

RESULT 9
AC073683 213137 bp DNA linear ROD 16-APR-2002
LOCUS Mus musculus chromosome 17 clone RP23-124G7, complete sequence.
DEFINITION AC073683
ACCESSION AC073683
VERSION AC073683.3 GI:20043100
KEYWORDS HTG.
SOURCE Mus musculus.

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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleaveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Ditya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, F., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabis, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyar, S., Hume, J., Johnson, B., Johnson, R., Jolivet, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebowitz, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Loreschewski, L., Louised, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., McNeill, T., Meenen, E., Milosavljevic, A., Minner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, N., Munidasa, M., Murphy, M., Nair, I., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankwelu, O., Okwodu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Plannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, P., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleccyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G. and Gibbs, R. A.

Direct Submission
Unpublished
2 (bases 1 to 142758)
Direct Submission
Worley, K. C.
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 142758)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GIWO
Center clone name: CH230-117J15

Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 6386 bases at least Q40
Consensus quality: 59524 bases at least Q30
Consensus quality: 73620 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1051: contig of 1051 bp in length
1151: gap of unknown length
1152 2422: contig of 1271 bp in length
2423 2522: gap of unknown length
2523 3765: contig of 1243 bp in length
3766 3865: gap of unknown length
3866 4876: contig of 1011 bp in length
4877 4976: gap of unknown length
4977 6421: contig of 1445 bp in length
6422 6521: gap of unknown length
6522 7566: contig of 1045 bp in length
7567 7666: gap of unknown length
7667 8715: contig of 1048 bp in length
8716 9992: contig of 1178 bp in length
9993 10092: gap of unknown length
10093 11721: contig of 1629 bp in length
11722 11821: gap of unknown length
11822 12916: contig of 1095 bp in length
12917 13016: gap of unknown length
13017 14068: contig of 1052 bp in length
14069 14168: gap of unknown length
14169 15291: contig of 1123 bp in length
15292 15391: gap of unknown length
15392 16534: contig of 1143 bp in length
16535 16634: gap of unknown length
16635 17883: contig of 1249 bp in length
17884 19034: contig of 1071 bp in length
19035 19134: gap of unknown length
19135 20588: contig of 1434 bp in length
20589 21775: gap of unknown length
21776 21875: gap of unknown length
21876 22977: contig of 1102 bp in length
22978 23077: gap of unknown length
23078 24103: contig of 1026 bp in length
24104 25215: gap of unknown length
25216 25316: contig of 1012 bp in length
25317 26384: contig of 1049 bp in length
26385 26464: gap of unknown length
26465 27655: contig of 1191 bp in length
27656 27755: gap of unknown length
27756 29418: contig of 1662 bp in length
29419 31140: contig of 1623 bp in length
31141 32270: contig of 1030 bp in length
32271 32370: gap of unknown length
32371 34165: contig of 1795 bp in length
34166 34265: gap of unknown length
34266 35438: contig of 1173 bp in length
35439 35538: gap of unknown length
35539 36965: contig of 1427 bp in length
36966 37065: gap of unknown length
37066 38188: contig of 1123 bp in length
38189 38288: gap of unknown length
38289 39399: contig of 1111 bp in length
39400 39499: gap of unknown length
39500 41093: contig of 1594 bp in length
41094 41193: gap of unknown length
41194 42376: contig of 1183 bp in length
42377 42476: gap of unknown length

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